论文

山东地区丙型肝炎病毒基因型及相关因素分析

徐皖苏，刘靓雯，秦晓华，刘宗清

济南市传染病医院中心实验室，　济南 250021

摘要：

目的　探索山东地区丙型肝炎病毒（HCV）基因分型及其相关关系。方法　采用基因芯片技术检出了448例HCV感染者的血清HCV基因型，同时检测了其中388例血清HCV RNA的含量，并对HCV基因型与HCV感染者的性别、年龄和HCV RNA含量进行了相关性分析。结果　检测到4种基因亚型（1a、1b、2a、3b），呈8种组合；其中1b和2a亚型多见，分别占61.2 %（274例）和 32.8%（147例）。Logistic多因素分析表明，基因1b型与HCV高病毒载量独立相关。结论　山东地区HCV基因分型以1b型为主，且与HCV高病毒载量相关。

关键词：　肝炎病毒，丙型；核糖核酸，丙型肝炎病毒；基因型

Genotypes and related factors of hepatitis C virus in patients infected with HCV in the Shandong area

XU Wan　su, Liu Jing　wen, Qin Xiao　hua, Liu Zong　qing

The Lenter Labovatory of Jinan Infectious Disease Hospital,　Jinan 250021,　China

Abstract:

Objective　To explore the distribution and related factors of hepatitis C virus (HCV) genotypes.　Methods　HCV genotypes were detected using gene chip assay in 448 patients who were infected with HCV.　HCV RNA levels were quantified by real-time PCR in 388/448 patients. The correlation between HCV genotypes and each variable (including gender,　age, the HCV level) was analyzed. Results　4 HCV genotypes (1a, 1b, 2a and 3b) and 4 mixed genotypes (1b+2a，1a+1b，1a+1b+2a，1b+3b) were found; of these 1b and 2a were the more common genotypes,　accounting for 61.2% and 32.8% respectively.　Logistic regression analysis indicated that genotype 1b independently correlated with high serum HCV RNA level.　Conclusion　HCV genotype 1b predominates in patients with HCV infection in the Shandong area,　correlating with high serum HCV RNA level.

Keywords: Hepatitis C virus;　Hepatitis C virus RNA;　Genotype

通讯作者:

作者简介: 徐皖苏（1962—　），女，副主任技师，主要从事病毒性肝炎分子生物学研究。　E-mail:xuwansu@163.com

作者Email:

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